



SEQUENCE LISTING

<110> Lelias, Renaud
Lebrun, Marc-Henri
Zundel, Jean-Luc
Effantin, Géraldine
Morin, Valérie

<120> Use of inhibitors of ketol-acid reductoisomerase to prevent or treat fungal infection of plants

<130> A36156-PCT-USA-A 072667.0196

<140> 10/797,248
<141> 2004-03-10

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<223> Putative mitochondrial transit peptide

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35 40 45

Ile Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val
50 55 60

Trp Glu Arg Ala Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys
65 70 75 80

Asp Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln
85 90 95

Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg
100 105 110

Lys Asp Gly Lys Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro
115 120 125

Gly Lys Asn Leu Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val
130 135 140

Ile Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala

145	150	155	160
Leu Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly			
165	170	175	
Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp			
180	185	190	
Val Asp Val Ile Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg			
195	200	205	
Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr			
210	215	220	
Gln Asp Val Thr Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val			
225	230	235	240
Ala Ile Gly Ser Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val			
245	250	255	
Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Ile His			
260	265	270	
Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser			
275	280	285	
Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu			
290	295	300	
Tyr Pro Leu Ile Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys			
305	310	315	320
Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys			
325	330	335	
Asp Ala Leu Lys Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp			
340	345	350	
Gly Ser Glu Thr Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr			
355	360	365	
Arg Glu Lys Tyr Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile			
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Trp Arg Ala Gly Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys			
385	390	395	400
Gln Lys			

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<213> *Saccharomyces cerevisiae*

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<223> mitochondrial transit peptide

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<308> gb:X04969

<309> 1993-09-12

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35 40 45

Lys Gln Ile Asn Phe Gly Gly Thr Val Glu Thr Val Tyr Glu Arg Ala
50 55 60

Asp Trp Pro Arg Glu Lys Leu Leu Asp Tyr Phe Lys Asn Asp Thr Phe
65 70 75 80

Ala Leu Ile Gly Tyr Gly Ser Gln Gly Tyr Gly Gln Gly Leu Asn Leu
85 90 95

Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Ala
100 105 110

Ser Trp Lys Ala Ala Ile Glu Asp Gly Trp Val Pro Gly Lys Asn Leu
115 120 125

Phe Thr Val Glu Asp Ala Ile Lys Arg Gly Ser Tyr Val Met Asn Leu
130 135 140

Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Ile Lys Pro Leu
145 150 155 160

Leu Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val
165 170 175

Phe Lys Asp Leu Thr His Val Glu Pro Pro Lys Asp Leu Asp Val Ile
180 185 190

Leu Val Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Lys
195 200 205

Glu Gly Arg Gly Ile Asn Ser Ser Tyr Ala Val Trp Asn Asp Val Thr
210 215 220

Gly Lys Ala His Glu Lys Ala Gln Ala Leu Ala Val Ala Ile Gly Ser
225 230 235 240

Gly Tyr Val Tyr Gln Thr Thr Phe Glu Arg Glu Val Asn Ser Asp Leu
245 250 255

Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu
260 265 270

Ala Gln Tyr Asp Val Leu Arg Glu Asn Gly His Ser Pro Ser Glu Ala
275 280 285
Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile
290 295 300
Gly Lys Tyr Gly Met Asp Tyr Met Tyr Asp Ala Cys Ser Thr Thr Ala
305 310 315 320
Arg Arg Gly Ala Leu Asp Trp Tyr Pro Ile Phe Lys Asn Ala Leu Lys
325 330 335
Pro Val Phe Gln Asp Leu Tyr Glu Ser Thr Lys Asn Gly Thr Glu Thr
340 345 350
Lys Arg Ser Leu Glu Phe Asn Ser Gln Pro Asp Tyr Arg Glu Lys Leu
355 360 365
Glu Lys Glu Leu Asp Thr Ile Arg Asn Met Glu Ile Trp Lys Val Gly
370 375 380
Lys Glu Val Arg Lys Leu Arg Pro Glu Asn Gln
385 390 395

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<309> 1996-05-23

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35 40 45

Gln Gln Val Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu
50 55 60

Glu Val His Glu Arg Ala Asp Trp Pro Ala Glu Lys Leu Leu Asp Tyr
65 70 75 80

Phe Lys Asn Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His
85 90 95

Gly Gln Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Val Gly

100 105 110

Val Arg Lys Asn Gly Lys Ser Trp Glu Asp Ala Ile Gln Asp Gly Trp
115 120 125

Val Pro Gly Lys Asn Leu Phe Asp Val Asp Glu Ala Ile Ser Arg Gly
130 135 140

Thr Ile Val Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp
145 150 155 160

Pro His Ile Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser
165 170 175

His Gly Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro
180 185 190

Thr Asp Val Asp Val Ile Leu Val Ala Pro Lys Gly Ser Gly Arg Thr
195 200 205

Val Arg Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala
210 215 220

Val Tyr Gln Asp Val Thr Gly Lys Ala Lys Glu Lys Ala Val Ala Leu
225 230 235 240

Gly Val Ala Val Gly Ser Gly Tyr Leu Tyr Glu Thr Thr Phe Glu Lys
245 250 255

Glu Val Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly
260 265 270

Ile His Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly
275 280 285

His Ser Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln
290 295 300

Ser Leu Tyr Pro Leu Ile Gly Ala His Gly Met Asp Trp Met Phe Asp
305 310 315 320

Ala Cys Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Thr Pro Lys
325 330 335

Phe Lys Asp Ala Leu Lys Pro Val Phe Asn Asn Leu Tyr Asp Ser Val
340 345 350

Lys Asn Gly Asp Glu Arg Lys Arg Ser Leu Glu Tyr Asn Ser Gln Pro
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Gly	Phe	Ser	Lys	Ala	Leu	Arg	Pro	Met	Ala	Arg	Gln	Leu	Ala	Thr	Pro
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gcc	gtt	cag	agg	cgt	acc	ttc	gtg	gct	gct	tct	agc	atg	gtg	cgg	gcc	151
Ala	Val	Gln	Arg	Arg	Thr	Phe	Val	Ala	Ala	Ser	Ser	Met	Val	Arg	Ala	
25				25				30					35			

acc	agg	aaa	gcc	gcc	gtc	gct	ccc	act	cag	cag	cag	atc	cgt	ggt	gtc	199
Thr	Arg	Lys	Ala	Ala	Val	Ala	Pro	Thr	Gln	Gln	Gln	Ile	Arg	Gly	Val	
40				40				45				50				

aag	acc	atg	gtt	gct	ggc	cac	aag	gag	cag	gtc	tgg	gag	cgt	gcc	247
Lys	Thr	Met	Asp	Phe	Ala	Gly	His	Lys	Glu	Gln	Val	Trp	Glu	Arg	Ala
55				55				60				65			

gac	tgg	ccc	aag	gag	aag	ctg	ctg	gag	tac	ttc	aag	gac	gac	acc	ctt	295
Asp	Trp	Pro	Lys	Glu	Lys	Leu	Leu	Glu	Tyr	Phe	Lys	Asp	Asp	Thr	Leu	
70				70				75			80					

gcc	ctc	atc	ggc	tat	ggt	tcg	cag	ggc	cac	ggc	cag	ggt	ctt	aac	ctc	343
Ala	Leu	Ile	Gly	Tyr	Gly	Ser	Gln	Gly	His	Gly	Gln	Gly	Leu	Asn	Leu	
85				85				90			95		100			

cgc	gac	aac	ggc	ctc	aac	gtc	atc	atc	ggt	gtg	cgc	aag	gac	gga	aag	391
Arg	Asp	Asn	Gly	Leu	Asn	Val	Ile	Ile	Gly	Val	Arg	Lys	Asp	Gly	Lys	
105				105				110			115					

tcg	tgg	aag	gac	gcc	gtc	cag	gac	ggc	tgg	gtt	ccc	ggc	aag	aac	ctc	439
Ser	Trp	Lys	Asp	Ala	Val	Gln	Asp	Gly	Trp	Val	Pro	Gly	Lys	Asn	Leu	
120				120				125			130					

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Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val Ile Met Asn Leu		
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ctg agc gac gct gcc cag agc gag acg tgg cct gct ctg aag ccc cag		535
Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Leu Lys Pro Gln		
150	155	160
atc act aag ggc aag act ctc tac ttc tcg cac ggt ttc tct ccc gtc		583
Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val		
165	170	175
ttc aag gac ctc acc aag gtc gag gtc ccc acc gac gtc gac gtc atc		631
Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp Val Asp Val Ile		
185	190	195
ctc tgc gcc ccc aag ggc tcc ggc cgc act gtc cgc tcg ctc ttc cgc		679
Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Arg		
200	205	210
gag ggt cgt ggc atc aac tcc tcc ttc gcc gtc tac cag gac gtg act		727
Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr Gln Asp Val Thr		
215	220	225
ggc gag gct gaa gag aag gct atc gct ctc ggt gtt gcc att ggc agt		775
Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val Ala Ile Gly Ser		
230	235	240
ggt tac ctc tac aag acc acc ttc gag aag gag gtc tac tct gac ctg		823
Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val Tyr Ser Asp Leu		
245	250	255
tac ggt gag cgt ggc tgc ctg atg ggt ggt atc cac ggt atg ttc ctt		871
Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu		
265	270	275
gcc cag tac gag gtt ctc cgc gag cgt ggc cac agc ccc tcg gag gct		919
Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser Pro Ser Glu Ala		
280	285	290
ttc aac gag act gtc gag gag gcc acc cag tct ctc tac ccc ctg atc		967
Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile		
295	300	305
ggt gcc aac ggc atg gac tgg atg tac gag gcc tgc tct acc act gct		1015
Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys Ser Thr Thr Ala		
310	315	320
cgt cgt ggt gcc att gac tgg agc ccc cgc ttc aag gac gcc ctc aag		1063
Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys Asp Ala Leu Lys		
325	330	335
ccc gtc ttc aac cag ctc tac gac tcg gtc aag gac ggc tct gag act		1111
Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp Gly Ser Glu Thr		
345	350	355
cag cgc tcg ctc gac tac aac agc cag ccc gac tac cgc gag aag tac		1159
Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr Arg Glu Lys Tyr		
360	365	370

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gag gcc gag atg gag gag atc cgc aac ctg gag atc tgg agg gcg ggt 1207
Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile Trp Arg Ala Gly
      375          380          385

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aag gct gtg cgc agc ctc cgt cct gag aac cag aag taa actgttatatt 1256
Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys
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      20          25          30
Met Val Arg Ala Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln
      35          40          45
Ile Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val
      50          55          60
Trp Glu Arg Ala Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys
      65          70          75          80

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Asp	Asp	Thr	Leu	Ala	Leu	Ile	Gly	Tyr	Gly	Ser	Gln	Gly	His	Gly	Gln
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Gly	Leu	Asn	Leu	Arg	Asp	Asn	Gly	Leu	Asn	Val	Ile	Ile	Gly	Val	Arg
						100			105						110
Lys	Asp	Gly	Lys	Ser	Trp	Lys	Asp	Ala	Val	Gln	Asp	Gly	Trp	Val	Pro
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Gly	Lys	Asn	Leu	Phe	Glu	Val	Asp	Glu	Ala	Ile	Ser	Arg	Gly	Thr	Val
						130			135						140
Ile	Met	Asn	Leu	Leu	Ser	Asp	Ala	Ala	Gln	Ser	Glu	Thr	Trp	Pro	Ala
						145			150						160
Leu	Lys	Pro	Gln	Ile	Thr	Lys	Gly	Lys	Thr	Leu	Tyr	Phe	Ser	His	Gly
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Phe	Ser	Pro	Val	Phe	Lys	Asp	Leu	Thr	Lys	Val	Glu	Val	Pro	Thr	Asp
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Val	Asp	Val	Ile	Leu	Cys	Ala	Pro	Lys	Gly	Ser	Gly	Arg	Thr	Val	Arg
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Ser	Leu	Phe	Arg	Glu	Gly	Arg	Gly	Ile	Asn	Ser	Ser	Phe	Ala	Val	Tyr
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Gln	Asp	Val	Thr	Gly	Glu	Ala	Glu	Glu	Lys	Ala	Ile	Ala	Leu	Gly	Val
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Ala	Ile	Gly	Ser	Gly	Tyr	Leu	Tyr	Lys	Thr	Thr	Phe	Glu	Lys	Glu	Val
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Tyr	Ser	Asp	Leu	Tyr	Gly	Glu	Arg	Gly	Cys	Leu	Met	Gly	Gly	Ile	His
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Gly	Met	Phe	Leu	Ala	Gln	Tyr	Glu	Val	Leu	Arg	Glu	Arg	Gly	His	Ser
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Pro	Ser	Glu	Ala	Phe	Asn	Glu	Thr	Val	Glu	Glu	Ala	Thr	Gln	Ser	Leu
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Ser	Thr	Thr	Ala	Arg	Arg	Gly	Ala	Ile	Asp	Trp	Ser	Pro	Arg	Phe	Lys
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Asp	Ala	Leu	Lys	Pro	Val	Phe	Asn	Gln	Leu	Tyr	Asp	Ser	Val	Lys	Asp
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Arg	Glu	Lys	Tyr	Glu	Ala	Glu	Met	Glu	Glu	Ile	Arg	Asn	Leu	Glu	Ile
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actccagcaca ctcatcgatcc gtgaacaggc cggcttagtcc tcgctccatcg agcagacgct 3780
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<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: primer 1

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<210> 10

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